

**PHARMACEUTICAL COMPOSITIONS COMPRISING  
HERPES VIRUS ENTRY RECEPTOR PROTEIN**

**Cross-Reference to Related Applications**

This application is a continuation of U.S. Application No. 09/333,279, which is a divisional of U.S. Application No. 08/509,024, filed on July 28, 1995, both of which are herein incorporated by reference in their entireties.

**Government Support**

This invention was made in part using funds obtained from the U.S. Government (National Institutes of Health Grant Nos. RO1 AI36293 and F32HI09022) and the U.S. Government may have certain rights in the invention.

**Technical Field of the Invention**

The field of this invention is a herpes virus entry receptor (HVEM). More particularly, the field of the present invention is recombinant mammalian HVEM, polynucleotides encoding that HVEM, and methods of making recombinant HVEM.

**Background of the Invention**

Glycosaminoglycan chains on cell surface proteoglycans serve as receptors for the binding of herpes simplex virus types 1 and 2 (HSV-1 and HSV-2) to cells. Binding is not sufficient for entry, however: other cell surface components are necessary for virus entry, which occurs by fusion of the virion envelope with a cell membrane. For example, Chinese hamster ovary (CHO) cells express glycosaminoglycan chains to which HSV-1 and HSV-2 can bind, but are resistant to the entry of some HSV strains, particularly HSV-1(KOS).

The present invention is directed to a newly discovered protein that enables herpes simplex virus (HSV) to penetrate into cells and is a previously undiscovered member of the family of receptors designated the tumor necrosis factor receptor/nerve growth factor receptor (TNFR/NGFR) family. Members of this family have characteristic repeats of amino acid sequence containing multiple cysteines and serve as receptors for a variety of

specific ligands, including but not limited to cytokines. The protein is designated herpes virus entry receptor protein or HVEM.

By identifying the gene that encodes HVEM, by showing that HVEM can mediate the entry of HSV into cells and by performing experiments to define viral and cell factors that influence the ability of HVEM to mediate HSV entry, the inventors have provided the knowledge and biological material required (i) to develop antiviral drugs that can act to block HSV (and perhaps other herpesvirus) entry into cells; (ii) to identify other members of the TNFR/NGFR family (or other cell surface molecules) that can serve as receptors for HSV-1, HSV-2 or other herpesviruses; (iii) to identify the natural ligand for the receptor, and (iv) to develop therapeutic approaches for enhancing or inhibiting action of the ligand on the receptor, depending on the pathologic or, beneficial consequences of this action.

### **Brief Summary of the Invention**

In one aspect, the present invention provides an isolated and purified polynucleotide comprising a nucleotide sequence consisting essentially of the nucleotide of SEQ ID NO:1 from about nucleotide position 294 to about nucleotide position 1142; (b) sequences that are complementary to the sequences of (a), and (c) sequences that, when expressed, encode a polypeptide encoded by a sequence of (a). A preferred polynucleotide is a DNA molecule. In another embodiment, the polynucleotide is an RNA molecule. A preferred polynucleotide is SEQ ID NO:1.

In another embodiment, a DNA molecule of the present invention is contained in an expression vector. The expression vector preferably further comprises an enhancer-promoter operatively linked to the polynucleotide. In an especially preferred embodiment, the DNA molecule has the nucleotide sequence of SEQ ID NO:1 from about nucleotide position 294 to about nucleotide position 1142.

In another aspect, the present invention provides an oligonucleotide of from about 15 to about 50 nucleotides containing a nucleotide sequence of at least 15 nucleotides that is identical or complementary to a contiguous sequence of a polynucleotide of this invention. A preferred oligonucleotide is an antisense oligonucleotide that is complementary to a portion of the polynucleotide of SEQ ID NO:1.

The present invention also provides a pharmaceutical composition comprising a polypeptide or an antisense oligonucleotide of this invention and a physiologically acceptable diluent.

In another aspect, the present invention provides an HVEM polypeptide of mammalian origin. In one embodiment, that HVEM is an isolated and purified polypeptide of about 300 amino acid residues and comprises the amino acid residue sequence of SEQ ID NO:2. More preferably, an HVEM of the present invention is a recombinant human HVEM.

In another aspect, the present invention provides a process of making HVEM comprising transforming a host cell with an expression vector that comprises a polynucleotide of the present invention, maintaining the transformed cell for a period of time sufficient for expression of the HVEM and recovering the HVEM. Preferably, the host cell is an eukaryotic host cell such as a mammalian cell or a bacterial cell. An especially preferred host cell is a mammalian ovarian cell. The present invention also provides an HVEM made by a process of this invention. A preferred such HVEM is recombinant human HVEM.

The present invention still further provides for a host cell transformed with a polynucleotide or expression vector of this invention. Preferably, the host cell is a mammalian cell such as an ovarian cell.

### **Brief Description of the Drawings**

In the drawings, which form a portion of the specification:

FIG. 1 shows a map of the plasmid (pBEC580) cloned from the cDNA library on the basis of its ability to convert resistant CHO-K1 cells to susceptibility to HSV-1(KOS) infection. The cDNA insert prepared as described in the text was ligated between BstXI and Not I sites in the polylinker region of pcDNA1 (shown in the inset).

FIG. 2A-2B shows the nucleotide sequence of HVEM cDNA (SEQ ID NO:1) and amino acid sequence (SEQ ID NO:2) of the open reading frame. The nucleotide sequence of the cDNA insert of pBEC580 was determined as shown. Analysis of the sequence revealed the presence of a single open reading frame, the translation of which is shown below the nucleotide sequences. Features of the 283 amino acid open reading frame include a signal peptide (dashed underline), two potential sites for the addition of N-linked carbohydrate (white underline) and a hydrophobic region predicted to be a membrane spanning domain (black underline). Also indicated by the shaded amino acid sequences are

the three complete and one partial cysteine rich repeats characteristic of members of the TNF/NGF receptor family.

FIG. 3 shows a map of the plasmid (pBEC10) produced by transferring the cDNA insert of pBEC580 to the vector, pcDNA3 (shown in the inset). The cDNA insert was excised from pBEC580 by cutting with HindIII and XhoI and was ligated to pcDNA3 that had also been cut with HindIII and XhoI. The position of the cytomegalovirus promoter (P-CMV) is shown and also the position of the selectable marker Neo, along with upstream and downstream sequences required for its expression in eukaryotic cells.

FIG. 4A-4B shows susceptibility of HeLa cells and various CHO cell lines to infection by HSV-1(KOS). The values reported are the optical density at 410 nm. Each point represents the mean of triplicate (FIG. 4A) or quadruplicate (FIG. 4B) determinations. The individual values were within 10% of the mean. FIG. 4A, HeLa cells (open circles) and CHO-K1 cells (closed circles). FIG. 4B, CHO cells lines stably transfected with pBEC10, which carries the HVEM cDNA [CHO-A3 (closed triangles); CHO-A12 (open squares); CHO-B3 (open triangles); CHO-B9 (closed squares); CHO-B11 (open circles)] and a control cell line stably transfected with the vector pcDNA3 [CHO-C8 (closed circles)].

FIG. 5 shows replication of three HSV strains in CHO cells stably transfected with HVEM and in control CHO cells and HeLa cells. Cells plated in 6-well plates at about  $5 \times 10^6$  cells per well were inoculated with the virus indicated at  $10^8$  PFU per well, to ensure that all susceptible cells were synchronously infected. After allowing 2 hr for virus binding and entry, the cells were washed and treated with citrate buffer, pH3, to inactivate input virus that bound to cells but failed to initiate infection. Culture medium was added and one set of cultures harvested immediately (2 hr after addition of the virus inoculum) for quantitation of infectious virus by plaque assay on Vero cells, to determine the baseline viral titer prior to the appearance of progeny virus (black bars). The remainder of the cultures were harvested at 31 hr for quantitation of viral progeny (diagonal-hatched bars). The values presented represent half the yield from each culture.

FIG. 6A-6B shows CHO-A12 cells that express HSV-1 or HSV-2 gD are resistant to HSV-1(KOS) infection. The results shown are for the amount of plasmid DNA giving maximal interference ( $1.5 \mu\text{g}$  per well for the gD-1 expressing plasmid and  $2.0 \mu\text{g}$  per well for the gD-2 expressing plasmid). The control plasmid was used at  $1.5 \mu\text{g}$  per well and the CHO-K1 cells were not transfected. The values given are the means of quadruplicate determinations.

FIG. 7 shows a map of the plasmid (pBL58) expressing the HVEM-Fc hybrid protein.

FIG. 8A-8C shows the nucleotide sequence (SEQ ID NO:6) of pBL58 and the amino acid sequence (SEQ ID NO:7) of the open reading frame encoding HVEM-Fc. Features of the HVEM ectodomain that were described in FIG. 2A-2B are shown here along with the site at which the HVEM sequence is fused to the rabbit IgG heavy chain sequence (the boxed residues are three amino acids inserted at the fusion site due to the EcoRI linker added). The two potential sites for the addition of N-linked glycans in HVEM are underlined along with a third site in the IgG sequence.

FIG. 9 shows a schematic drawing of human HVEM. The protein has characteristics of a typical type I membrane glycoprotein, including an N-terminal signal sequence (diagonal-hatched box) and a membrane-spanning region (cross-hatched box). The protein also has the cysteine-rich repeats characteristic of the TNFR/NGFR family of cell surface receptors. Each repeat has 4-6 cysteine residues (represented by vertical lines).

FIG. 10 shows the relative susceptibilities of A12 cells transfected with various gD-expressing plasmids.

## **Detailed Description of the Invention**

### **I. The Invention**

The present invention provides isolated and purified polynucleotides that encode HVEM of mammalian origin, expression vectors containing those polynucleotides, host cells transformed with those expression vectors, a process of making HVEM using those polynucleotides and vectors, and isolated and purified HVEM.

### **II. HVEM Polynucleotides**

In one aspect, the present invention provides an isolated and purified polynucleotide that encodes an HVEM polypeptide of mammalian origin.

A polynucleotide of the present invention that encodes HVEM is an isolated and purified polynucleotide that comprises a nucleotide sequence consisting essentially of the nucleotide sequence of SEQ ID NO:1 from about nucleotide position 294 to about nucleotide position 1142 of SEQ ID NO:1, (b) sequences that are complementary to the sequences of (a), and (c) sequences that, when expressed, encode a polypeptide encoded by

the sequences of (a). A preferred polynucleotide is a DNA molecule. In another embodiment, the polynucleotide is an RNA molecule.

A nucleotide sequence and deduced amino acid residue sequence of human HVEM are set forth in FIG. 2A-2B. The nucleotide sequence of SEQ ID NO:1 in FIG. 2A-2B is a full length DNA clone of human HVEM. SEQ ID NO:2 in FIG. 2A-2B is the deduced amino acid residue sequence of that clone.

The present invention also contemplates DNA sequences which hybridize under stringent hybridization conditions to the DNA sequences set forth above. Stringent hybridization conditions are well known in the art and define a degree of sequence identity greater than about 70%-80%. The present invention also contemplates naturally occurring allelic variations and mutations of the DNA sequences set forth above so long as those variations and mutations code, on expression, for an HVEM of this invention as set forth hereinafter.

As set forth above, SEQ ID NO:1, is a full length cDNA clone of human HVEM. As is well known in the art, because of the degeneracy of the genetic code, there are numerous other DNA and RNA molecules that can code for the same polypeptide as those encoded by SEQ ID NO:1. The present invention, therefore, contemplates those other DNA and RNA molecules which, on expression, encode for the polypeptide encoded by SEQ ID NO:1. Having identified the amino acid residue sequence of HVEM, and with knowledge of all triplet codons for each particular amino acid residue, it is possible to describe all such encoding RNA and DNA sequences. DNA and RNA molecules other than those specifically disclosed herein and, which molecules are characterized simply by a change in a codon for a particular amino acid are within the scope of this invention.

A Table of codons representing particular amino acids is set forth below in

Table 1.

TABLE 1					
First position (5' end)	Second Position				Third position (3' end)
	T/U	C	A	G	
	Phe	Ser	Tyr	Cys	T/U
	Phe	Ser	Tyr	Cys	C
T/U	Leu	Ser	Stop	Stop	A
	Leu	Ser	Stop	Trp	G
	Leu	Pro	His	Arg	T/U
	Leu	Pro	His	Arg	C
C	Leu	Pro	Gln	Arg	A
	Leu	Pro	Gln	Arg	G
	Ile	Thr	Asn	Ser	T/U
	Ile	Thr	Asn	Ser	C
A	Ile	Thr	Lys	Arg	A
	Met	Thr	Lys	Arg	G
	Val	Ala	Asp	Gly	T/U
	Val	Ala	Asp	Gly	C
G	Val	Ala	Glu	Gly	A
	Val	Ala	Glu	Gly	G

A simple change in a codon for the same amino acid residue within a polynucleotide will not change the structure of the encoded polypeptide. By way of example, it can be seen from SEQ ID NO:1 (see FIG. 2A-2B) that a CCT codon for proline exists at nucleotide positions 300-302. It can also be seen from that same sequence, however, that proline can be encoded by a CCC codon (see e.g., nucleotide positions 324-

326). Substitution of the latter CCC codon for proline with the CCT codon for proline, or vice versa, does not substantially alter the DNA sequence of SEQ ID NO:1 and results in expression of the same polypeptide. In a similar manner, substitutions of codons for other amino acid residues can be made in a like manner without departing from the true scope of the present invention.

A polynucleotide of the present invention can also be an RNA molecule. A RNA molecule contemplated by the present invention is complementary to or hybridizes under stringent conditions to any of the DNA sequences set forth above. As is well known in the art, such a RNA molecule is characterized by the base uracil in place of thymidine. Exemplary and preferred RNA molecules are mRNA molecules that encode an HVEM of this invention.

The present invention also contemplates oligonucleotides from about 15 to about 50 nucleotides in length, which oligonucleotides serve as primers and hybridization probes for the screening of DNA libraries and the identification of DNA or RNA molecules that encode HVEM. Such primers and probes are characterized in that they will hybridize to polynucleotide sequences encoding HVEM or related receptor proteins. An oligonucleotide probe or primer contains a nucleotide sequence of at least 15 nucleotides that is identical to or complementary to a contiguous sequence of an HVEM polynucleotide of the present invention. Thus, where an oligonucleotide probe is 25 nucleotides in length, at least 15 of those nucleotides are identical or complementary to a sequence of contiguous nucleotides of an HVEM polynucleotide of the present invention. Exemplary HVEM polynucleotides of the present invention are set forth above.

A preferred oligonucleotide is an antisense oligonucleotide. The present invention provides a synthetic antisense oligonucleotide of less than about 50 nucleotides, preferably less than about 35 nucleotides, more preferably less than about 25 nucleotides and most preferably less than about 20 nucleotides. An antisense oligonucleotide of the present invention is directed against a DNA or RNA molecule that encodes HVEM. Preferably, the antisense oligonucleotide is directed against the protein translational initiation site or the transcriptional start site. In accordance with this preferred embodiment, an antisense molecule is directed against a region of SEQ. ID NO:1 from about nucleotide position 254 to about nucleotide position 334. It is understood by one of ordinary skill in the art that an antisense oligonucleotide can be directed either against a DNA or RNA sequence that encodes a specific target. Thus, an antisense oligonucleotide of the present



invention can also be directed against polynucleotides that are complementary to those shown in SEQ. ID NO:1 as well as the equivalent RNA molecules.

Preferably, the nucleotides of an antisense oligonucleotide are linked by pseudophosphate bonds that are resistant to cleavage by exonuclease or endonuclease enzymes. Preferably the pseudophosphate bonds are phosphorothioate bonds. By replacing a phosphodiester bond with one that is resistant to the action of exo-and/or endonuclease, the stability of the nucleic acid in the presence of those enzymes is increased. As used herein, pseudophosphate bonds include, but are not limited to, methylphosphonate, phosphomorpholidate, phosphorothioate, phosphorodithioate and phosphoroselenoate bonds.

An oligonucleotide primer or probe, as well as an antisense oligonucleotide of the present invention can be prepared using standard procedures well known in the art. A preferred method of polynucleotide synthesis is via cyanoethyl phosphoramidite chemistry. A detailed description of the preparation, isolation and purification of polynucleotides encoding human HVEM is set forth below.

Briefly, CHO-K1 cells are resistant to the entry of HSV1(KOS). The present invention discloses an assay to screen for human cDNAs encoding proteins capable of conferring susceptibility to HSV1(KOS) infection on the CHO-K1 cells. Control and transfected CHO-K1 cells were exposed to a strain of HSV-1(KOS) that had been modified to express *E. coli* beta-galactosidase, under control of a human cytomegalovirus promoter, immediately after viral entry into a cell. Any transfected cells that became susceptible to HSV-1(KOS) entry expressed beta-galactosidase after infection. Addition of the appropriate beta-galactosidase substrate (X-gal) caused the infected cells to turn blue. The high level of resistance of the CHO-K1 cells to HSV-1(KOS) infection made it possible to detect very small numbers of cells rendered susceptible to infection by transfection of the human cDNAs.

A commercially obtained unidirectional cDNA library prepared from human HeLa cell mRNA was used for the transfections. The plasmids in this library express human proteins under control of the human cytomegalovirus promoter, after transfection into eukaryotic cells. The cDNA library was purchased from Invitrogen Corp (3985 B Sorrento Valley Blvd., San Diego, CA 92121):

catalog no.	A950-10
mRNA source	HeLa cells (a human cell line derived from a carcinoma)

primer	oligo dT(Not I)
vector	pcDNAI

This library was constructed using materials produced by Invitrogen according to the following protocol:

mRNA was isolated from the HeLa cells using the Invitrogen FastTrack® mRNA Isolation Kit. The mRNA was copied by AMV reverse transcriptase, using an oligo dT(NotI) primer, to produce the first strand of DNA. The sequence of this primer is 5'- d PO<sub>4</sub>[AACCCGGCTCGAGCGGCCGCT<sub>18</sub>]-3' (SEQ ID NO:3). The underlined sequence is the NotI site used in a later step for cleavage of the cDNA and its insertion into the vector in a directional fashion.

The product was converted to double-stranded DNA by DNA polymerase in combination with RNaseH, and *E. coli* DNA ligase. Any sticky (single-stranded) ends were made blunt (filled in) by use of T4 polymerase. A BstXI/EcoRI adapter was added to the ends by blunt-end ligation. The sequence of the adapter is: GAATTCCACCACACTTAAGGTG (SEQ ID NO.:4). The cDNA was cut with BstXI and NotI and cloned directionally by sticky-end ligation into pcDNAI, which had also been cut with BstXI and Not I.

The plasmids were used to transform *E. coli* strain MC1061/P3. The number of primary recombinant plasmids was estimated to be about  $1.5 \times 10^6$ . The number of colonies in the amplified library was  $4.5 \times 10^7$  per ml. The estimated size range of the inserts was 0.9 kb to 1.6 kb.

$1.5 \times 10^7$  bacteria were plated ( $1.5 \times 10^5$  bacteria per large Petri plate for a total of 100 plates) to allow the growth of bacterial colonies. The colonies were scraped from each plate to yield one pool of bacteria from each plate. Samples of the 100 bacterial pools were mixed to yield 10 mixtures of 10 pools each. Plasmid DNA was extracted from each mixture of pools by standard means.

Each plasmid DNA mixture was prepared with LipofectAMINE™ (GibcoBRL), according to the manufacturer's directions, for transfection into Chinese hamster ovary cells, strain K1 (CHO-K1).

To determine whether any of the transfected cells became susceptible to HSV-1(KOS) infection, the transfected cells and control cells (untransfected or transfected with irrelevant DNA) were exposed to a mutant form of HSV-1(KOS) at an input dose sufficiently high to infect all susceptible cells. This mutant is deleted for one of the essential

glycoproteins, gL, and must be propagated on gL-expressing Vero cells. The virus produced on the gL-expressing cells is fully infectious but can undergo only one round of replication because defective virus is produced in non-complementing cells. The gL open reading frame was replaced by the *E. coli* lacZ gene, downstream of the strong cytomegalovirus promoter. The lacZ gene encodes beta-galactosidase.

After exposure to virus for several hours, the transfected CHO-K1 cells were fixed and incubated with the beta-galactosidase substrate, X-gal. Susceptible cells were readily identified by their blue color resulting from conversion of the substrate to an insoluble blue preceipitate by the beta-galactosidase expressed after entry of the mutant HSV-1(KOS).

DNA from one mixture of ten pools was found to be positive for ability to convert some of the transfected CHO-K1 cells to susceptibility. Each of the ten bacterial pools in this mixture was tested separately by extracting plasmid DNA and repeating steps set forth above. Pool 82 was found to be positive.

Bacterial pool 82 was itself divided into 100 subpools as described above. It was found that subpool 53 was positive. The bacteria in subpool 53 were plated and 900 individual clones were picked and grown up. Plasmids DNAs were extracted from each of the clones for testing. Clone 580 was found to be positive. Clone 580 was designated pBECS80. A map of this plasmid is shown in FIG. 1.

The nucleotide sequence of the cDNA insert of pBECS80 was determined by use of the Sequenase® Kit (US Biochemical Corp) according to the manufacturer's instructions.

The PCgene suite of software from Intelligenetics, Inc. was used to analyze the nucleotide sequence. As shown in FIG. 2A-2B, one open reading frame was found in the correct orientation. The protein encoded in this open reading frame was designated a herpesvirus entry receptor protein (HVEM) and was found by sequence analysis to have properties of a type I membrane glycoprotein. Shown in FIG. 2A-2B are 1) the predicted signal peptide that could direct translocation of the nascent peptide across membranes of the rough endoplasmic reticulum; 2) two sites that are signals for the addition of N-linked carbohydrate; and 3) a hydrophobic region that is predicted to be a membrane-spanning region, adjacent to a very basic region which could serve to anchor the protein in a membrane.

The blastp and blastn programs were used to search databases maintained by the National Center for Biotechnology Information (NCBI), National Library of Medicine, National Institutes of Health, in Bethesda, MD, for proteins or nucleotide sequences that might be identical to, or related to, those of the cDNA insert. The blastp program was used to search for HVEM-related protein sequences in the database updated daily that contains non-redundant protein sequences from five component databases (Brookhaven Protein Data Bank, the SWISS-PROT database, The PIR database, the coding sequence translations from the GenBank databases and two other databases that contain cumulative weekly or daily updates, respectively, of the SWISS-PROT database and the translations from Gen Bank).

This search failed to detect any closely related proteins, indicating that HVEM has not been previously described. The blastp program identified about 30 proteins that share a characteristic sequence motif with HVEM, namely three or more cysteine-rich repeats with a characteristic pattern of 6 cysteine residues. These other proteins that are related to HVEM by this motif are all members of the TNF/NGF receptor family. They encode membrane receptors that can be triggered by the binding of specific ligands to activate specific pathways important to cell survival, apoptosis or induced protective responses against infectious agents or trauma.

The blastn program identified two entries in the DNA database (the combined non-redundant database consisting of nucleotide sequence entries from the Brookhaven Protein Data Bank, GenBank, the EMEL Data Library and cumulative daily updates of the GenBank and EMBL databases) that provide partial nucleotide sequence information for cDNAs that are very closely related to the cDNA encoding HVEM. One entry (locus HSC0BG042) provides partial sequence that is closely related to sequence in the 3' non-coding region of the HVEM cDNA. The other entry (locus HSC0BG041) provides partial sequence that is closely related to sequence in the 5' non-coding region and extending 43 amino acids into the N-terminal region of the HVEM open reading frame, but not extending into the TNF/NGF receptor motifs.

The cDNA insert was transferred to another vector, pcDNA3, which carries a selectable marker (the neomycin gene) that can be used to isolate cell lines stably carrying the plasmid. Cells that carry and express this gene are resistant to the toxic effects of a drug called G418. The cDNA insert of pBEC580 was excised by cutting with HindIII and XhoI and the insert was ligated to pcDNA3, which had also been cut with HindIII and XhoI, to produce the new plasmid called pBEC10. A map of pBEC10 is shown in FIG. 3.

CHO-K1 cells were transfected with pBEC10 or pcDNA3 and, after about 48 hours, incubated with medium containing G418. Only cells carrying the plasmid (with the Neo marker) were able to survive.

Several stably transformed colonies of cells were isolated after transfection with each plasmid and were cloned. None of the clones obtained with pcDNA3 were susceptible to HSV-1(KOS) infection. About half of the clones obtained with pBEC10 were susceptible (the resistant clones may not have been able to express the protein encoded in the cDNA insert). Cells plated in 96-well dishes, at densities ranging from  $10^4$  to  $5 \times 10^4$  cells per well, were exposed to HSV-1(KOS)gL86 in the quantities indicated. At 6 hr after the addition of virus, the cells were solubilized with detergent and beta-galactosidase substrate added to assess the efficiency of viral entry. Expression of beta-galactosidase signals that the virus has entered a cell and the amount of enzyme produced is proportional to the number of infected cells, at least until plateau values of beta-galactosidase activity are achieved. FIGs. 4A-4B and 5 show that CHO-K1 parental cells and CHO cells transfected with the control plasmid, pcDNA3, are resistant to HSV1(KOS) infection whereas the cells transfected with, and stably carrying pBEC10, are susceptible to HSV-1(KOS) infection.

Although the cells transfected with the HVEM cDNA are fully susceptible to infection by HSV-1(KOS), they are resistant to infection by a mutant of HSV-1(KOS), designated HSV-1(KOS)rid1, that differs from parental virus only by an amino acid substitution in the viral envelope glycoprotein gD. This indicates that gD, at least in part, determines the ability of virus to use HVEM for entry. Because HSV-1(KOS) expressing the mutant form of gD can infect human cells almost as efficiently as parental HSV-1(KOS), there must be cell surface molecules expressed in human cells, in addition to HVEM, that can be used for entry.

CHO-A12 cells in 6-well plates were transfected with plasmids that express HSV-1 gD (pRE4) or HSV-2 gD (pWW65) under control of the Rous sarcoma virus promoter or with a control plasmid consisting of the vector with no insert (pdH). These plasmids were obtained from G. Cohen and R. Eisenberg (Univ. of Pennsylvania). Transfection was done with the LipofectAMINE<sup>TM</sup> reagent (GibcoBRL) using plasmid quantities ranging from 0.5 to 2.5  $\mu$ g per well. At 24 hr after transfection, the cells were replated in 96-well plates and, 12 hr later, were exposed to HSV-1(KOS)gL86 to assess the susceptibility of the cells to infection.

Transfection of HVEM-expressing CHO cells with a plasmid that expresses wild-type gD (either the HSV-1 or HSV-2 forms of gD) confers resistance to infection by HSV-1(KOS) (See FIG. 6). This is an interference activity of gD that has been previously described. When gD is expressed by the cell, it can render a susceptible cell resistant to HSV-1 infection, possibly by sequestering a cell surface receptor needed for HSV-1 entry. The fact that gD expression renders the HVEM-expressing cells resistant to HSV-1(KOS) infection suggests that there may be a direct physical interaction between gD (both the HSV-1 and HSV-2 forms) and HVEM.

Table 2 below lists the cell lines obtained and summarizes some of their properties:

Cell line	Plasmid used for transfection	Susceptible to infection by:			
		HSV-1(KOS)	HSV-1(KOS)rid1	HSV-1(F)	HSV-2(333)
Cell lines obtained from others or from culture collections:					
HeLa (human)	None	Yes	Yes	Yes	Yes
Hep-2 (human)	None	Yes	Yes	Yes	Yes
CHO-K1(hamster)	None	No	No	Partially	Yes
New cell lines					
CHO-A3	pBEC10	Yes	N.T. <sup>a</sup>	N.T. <sup>a</sup>	N.T. <sup>a</sup>
CHO-A12 <sup>b</sup>	pBEC10	Yes	No <sup>c</sup>	Yes	Yes
CHO-B3	pBEC10	partially	N.T. <sup>a</sup>	N.T. <sup>a</sup>	N.T. <sup>a</sup>
CHO-B9	pBEC10	Yes	N.T. <sup>a</sup>	N.T. <sup>a</sup>	N.T. <sup>a</sup>
CHO-B11	pBEC10	Yes	N.T. <sup>a</sup>	N.T. <sup>a</sup>	N.T. <sup>a</sup>
CHO-C8	pcDNA3	No	No <sup>c</sup>	N.T. <sup>a</sup>	N.T. <sup>a</sup>

<sup>a</sup> N.T. -- Not tested.

<sup>b</sup> When the A12 cells were transfected with plasmids expressing HSV-1 or HSV-2 gD, they became resistant to HSV-1(KOS) infection.

<sup>c</sup> CHO-K1 cells are slightly more susceptible to infection by HSV-1(KOS)rid1 than by parental HSV-1(KOS) but the expression of HVEM in the transfected cells does not enhance susceptibility of the cells to HSV-1(KOS)rid1, in marked contrast to the results obtained with HSV-1(KOS).

Southern blots were done with digests of DNA from three human cell lines (Hep-2, HeLa and HT1080), one monkey cell line (Vero), the Chinese hamster ovary cell line used for cloning HVEM (CHO-K1) and two of the CHO cell lines stably transfected with pBEC10 (CHO-A12 and CHO-B9). The probes used to detect DNA fragments with

homology to HVEM were an EcoRI fragment of the HVEM cDNA insert that includes most of the insert and a smaller PvuII fragment that includes only the 3' end of the HVEM open reading frame and some of the on-coding sequence downstream. The results showed that: (i) all three human cell lines contain DNA homologous to HVEM with fragment sizes that are the same for all three cell lines in a single digest (different digests yield hybridizable bands of different sizes but the DNAs from three cell lines are indistinguishable); (ii) only a subset of the human DNA fragments that hybridize to the larger EcoRI fragment also hybridize to the smaller PvuII fragment; (iii) the monkey cells contain weakly hybridizable DNA fragments of different sizes from those found in the human DNAs; (iv) the parental CHO-K1 cells contain no hybridizable DNA fragments; (v) the stably transfected cell lines (CHO-A12 and CHO-B9) contain DNA homologous to HVEM as predicted.

The results obtained with the human, monkey and Chinese hamster DNAs confirm that HVEM is encoded by a human cDNA and indicate that the human HVEM gene is probably a single-copy gene with multiple introns and exons, perhaps extending over a large stretch of DNA. The results also indicate that monkey cells have a gene related to human HVEM. If Chinese hamster cells have an HVEM gene, its sequence has diverged too much to be detected by a human HVEM probe.

Poly-adenylated RNAs extracted from various human tissues (heart, brain, placenta, lung, liver, skeletal muscle, kidney, and pancreas) were obtained from Clontech, Inc., as samples that had already been fractionated by electrophoresis and transferred to a membrane. The membrane was used for hybridization with the larger EcoRI probe mentioned above (almost the entire HVEM cDNA insert). The results showed that there were variable amounts of RNA homologous to HVEM in all the samples. The largest amounts were found in lung and kidney. The sizes of the bands were about 1.8 and 3.8 kb. The HVEM cDNA insert claimed in the application is about 1.8 kb.

### III. HVEM Polypeptides

In another aspect, the present invention provides an HVEM polypeptide of mammalian origin. An HVEM of the present invention is a polypeptide of about 300 amino acid residues. Preferably, an HVEM is a human HVEM. A human form of HVEM is shown in SEQ ID NO:2. Thus, human HVEM can be defined as a polypeptide of about 293 or less amino acid residues comprising the amino acid residue sequence of SEQ ID NO:2.

The present invention also contemplates amino acid residue sequences that are substantially duplicative of the sequences set forth herein such that those sequences demonstrate like biological activity to disclosed sequences. Such contemplated sequences include those sequences characterized by a minimal change in amino acid residue sequence or type (e.g., conservatively substituted sequences) which insubstantial change does not alter the basic nature and biological activity of HVEM.

It is well known in the art that modifications and changes can be made in the structure of a polypeptide without substantially altering the biological function of that peptide. For example, certain amino acids can be substituted for other amino acids in a given polypeptide without any appreciable loss of function. In making such changes, substitutions of like amino acid residues can be made on the basis of relative similarity of side-chain substituents, for example, their size, charge, hydrophobicity, hydrophilicity, and the like.

As detailed in United States Patent No. 4,554,101, incorporated herein by reference, the following hydrophilicity values have been assigned to amino acid residues: Arg (+3.0); Lys (+3.0); Asp (+3.0); Glu (+3.0); Ser (+0.3); Asn (+0.2); Gln (+0.2); Gly (0); Pro (-0.5); Thr (-0.4); Ala (-0.5); His (-0.5); Cys (-1.0); Met (-1.3); Val (-1.5); Leu (-1.8); Ile (-1.8); Tyr (-2.3); Phe (-2.5); and Trp (-3.4). It is understood that an amino acid residue can be substituted for another having a similar hydrophilicity value (e.g., within a value of plus or minus 2.0) and still obtain a biologically equivalent polypeptide.

In a similar manner, substitutions can be made on the basis of similarity in hydropathic index. Each amino acid residue has been assigned a hydropathic index on the basis of its hydrophobicity and charge characteristics. Those hydropathic index values are: Ile (+4.5); Val (+4.2); Leu (+3.8); Phe (+2.8); Cys (+2.5); Met (+1.9); Ala (+1.8); Gly (-0.4); Thr (-0.7); Ser (-0.8); Trp (-0.9); Tyr (-1.3); Pro (-1.6); His (-3.2); Glu (-3.5); Gln (-3.5); Asp (-3.5); Asn (-3.5); Lys (-3.9); and Arg (-4.5). In making a substitution based on the hydropathic index, a value of within plus or minus 2.0 is preferred.

A comparison of the amino acid sequence SEQ ID No.2 with the protein databases maintained at the National Library of Medicine (NIH) and with a computer program designed to detect functional motifs in proteins revealed that HVEM has not previously been described, that it is not closely related to other proteins in the database, but that it has three copies of a cysteine-rich motif found in members of the TNFR/NGFR family.



heavy chain fragment. This latter fragment was prepared for the ligation by using PCR technology to insert an EcoRI site just upstream of the following rabbit sequence (ACAAGACCGTTGCACCCTC) (SEQ ID NO:5). Cleavage at this EcoRI site, followed by filling-in, permitted blunt-end ligation to the PvuII site of HVEM so that the two open reading frames were joined in the same reading frame. The 3' end of the rabbit cDNA insert was cut with PstI and joined to the HindIII site of pGEM4 by blunt-end ligation (the PstI cut end was trimmed and the HindIII cut end was filled in). The vector sequences are from pGEM4 and include sequences extending to a unique NheI site that was joined by sticky-end ligation to an SpeI site adjacent to the cytomegalovirus promoter (P-CMV) from pcDNAneo. The other end of the P-CMV region was cut with HindIII and is joined to the HindIII site at the top of the map (FIG. 7).

Expression of the hybrid protein has been demonstrated both in Vero cells and in CHO-K1 cells. The protein is secreted into the medium, as predicted, since it should have a signal sequence for translocation into the cell's secretory pathway but has no membrane-spanning region to anchor it to a membrane. The hybrid protein is readily detected on Western blots by use of commercially available antibodies specific for the constant regions of rabbit IgG.

Treatment of the hybrid protein with various glycosidases (endoH, endoF and endoO) has revealed that the protein carries N-linked glycans of the complex type, which is characteristic for secreted proteins, and also carries O-linked glycans, as predicted. This hybrid protein is used to screen for mouse monoclonal antibodies specific for HVEM and to identify HSV proteins with which it might interact.

The hybrid gene is contained in two different expression plasmids, the latter of which contains a selectable marker for obtaining transformed cells that stably carry the plasmid. Transfection of these including pGEM3, pGEM4 and pcDNAneo. Starting from the HindIII site of pBL58, part of the polylinker from pGEM3 (HindIII site to XbaI site) was linked to a sticky end created by cutting the HVEM insert with NheI about 37 nucleotides upstream of the HVEM start codon. Another cleavage of the HVEM insert at a PvuII site within the open reading frame created a blunt end that was blunt-end ligated to the rabbit IgG heavy chain fragment. This latter fragment was prepared for the ligation by using PCR technology to insert an EcoRI site just upstream of the following rabbit sequence (ACAAGACCGTTGCACCCTC) (SEQ ID NO:5). Cleavage at this EcoRI site, followed by filling-in, permitted blunt-end ligation to the PvuII site of HVEM so that the two open

reading frames were joined in the same reading frame. The 3' end of the rabbit cDNA insert was cut with PstI and joined to the HindIII site of pGEM4 by blunt-end ligation (the PstI cut end was trimmed and the HindIII cut end was filled in). The vector sequences are from pGEM4 and include sequences extending to a unique NbeI site that was joined by sticky-end ligation to an SpeI site adjacent to the cytomegalovirus promoter (P-CMV) from pcDNAneo. The other end of the P-CMV region was cut with HindIII and is joined to the HindIII site at the top of the map (See SEQ ID NO:6, FIGs. 8A and 8B).

Expression of the hybrid protein (SEQ. ID. NO:7, FIGs. 8A and 8B) has been demonstrated both in Vero cells and in CHO-K1 cells. The protein is secreted into the medium, as predicted, since it should have a signal sequence for translocation into the cell's secretory pathway but has no membrane-spanning region to anchor it to a membrane. The hybrid protein is readily detected on Western blots by use of commercially available antibodies specific for the constant regions of rabbit IgG.

Treatment of the hybrid protein with various glycosidases (endoH, endoF and endoO) has revealed that the protein carries N-linked glycans of the complex type, which is characteristic for secreted proteins, and also carries O-linked glycans, as predicted. This hybrid protein is used to screen for mouse monoclonal antibodies specific for HVEM and to identify HSV proteins with which it might interact.

The hybrid gene is contained in two different expression plasmids, the latter of which contains a selectable marker for obtaining transformed cells that stably carry the plasmid. Transfection of these plasmids into cells has revealed expression of a hybrid polypeptide of molecular weight approximately 60,000 after dissociation into its component chains.

This hybrid polypeptide, designated HVEM/Fc, carries N-linked glycans and is expressed as a dimer held together by disulfide bonds (this is characteristic of hybrid proteins prepared with IgG domains that can dimerize to form the Fc region). Commercially available antibodies specific for rabbit IgG were used to detect HVEM/Pc in Western blots and in ELISA assays.

The observed apparent size of the hybrid protein is similar to the size predicted, provided the predicted molecular weight includes about 10,000 for the added carbohydrate.

Evidence has been obtained that HVEM is only one of several cell surface receptors that can mediate the entry of HSV-1 and HSV-2 into cells and that functional use

of HVEM (and perhaps other receptors) is determined by the structure of the virion envelope glycoprotein gD. A mutant of HSV-1(KOS), designated HSV-1(KOS)rid1 has a single amino acid substitution in gD that confers resistance to gD-mediated interference with HSV infection and alters slightly the ability of this virus, relative to the wild-type parental strain, to penetrate into various cell types including CHO cells and human cells. By use of a mutant strain of HSV-1(KOS) that is deleted for gD and complemented by replication in cells expressing either the wild-type or mutant form of gD it has been shown that HVEM expression renders CHO cells fully susceptible to infection by virus carrying wild-type gD but not to infection by virus carrying mutant gD, despite the fact that both viruses could infect human cells with nearly equal efficiency. The implications of this result are several-fold.

First, the result shows that the structure of gD determines whether HVEM can be used as a receptor for entry, raising the possibility of a direct physical interaction. This is consistent with knowledge that gD is one of at least four envelope glycoproteins required for HSV entry. Second, although HVEM is expressed in cultured human cells, such as HeLa cells (the cDNA library used was prepared from HeLa cells), there must be other receptors expressed in human cells that can facilitate the entry of HSV-1(KOS) carrying the mutant form of gD. Third, because CHO-K1 cells are so resistant to HSV-1(KOS) carrying the rid1 form of gD, it is possible to use the gD-negative mutant of HSV-1(KOS), which expresses beta-galactosidase and can be complemented with the rid1 form of gD, to screen for expression of the human gene or genes that can facilitate the entry of HSV-1(KOS)rid1 into CHO-K1 cells.

The possibility exists that several members of the TNFR/NGFR family can serve as receptors for entry of HSV-1, HSV-2 or other herpesviruses, and that the particular receptor favored by a given herpesvirus or strain is determined at least in part by the structure of gD.

Expression of HVEM in CHO-K1 cells significantly enhances the entry of at least two HSV-1 strains. Because the original CHO cells are fully susceptible to entry of the HSV-2 strains tested, it is not possible to assess directly whether HVEM has any effect on HSV-2 entry into CHO-K1 cells. Cells expressing HSV gD become resistant, however, to HSV-1 and HSV-2 infection, and also to infection with related alphaherpesviruses, because of a block to penetration (binding is unimpaired by gD expression). This phenomenon has been called gD-mediated interference.

The fact that HSV-1 gD can interfere with infection by HSV-1, HSV-2 or other herpesviruses implies that all the herpesviruses may use an overlapping set of receptors for entry. Transient expression of gD in CHO cells already expressing HVEM renders the cells resistant to HSV-1(KOS) entry. Both the HSV-2 and HSV-1 forms of wild-type gD are able to interfere with ability of HSV-1(KOS) to use HVEM for entry, suggesting that both forms can interact with HVEM for interference and possibly also for entry. As predicted from the hypothesis about the mechanism of interference, the rid1 form of gD is impaired in ability to mediate interference in HVEM-expressing CHO cells (consistent with the finding that virus carrying the rid1 form of gD is impaired in ability to enter HVEM-expressing CHO cells).

The interference activity of gD can be quantitated by transfecting gD-expressin gplasmids into HVEM-expressing CHO cells and then exposing the cells to HSV-1(KOS)gL86 to determine whether the cells are susceptible or resistant to viral entry. This provides an assay for testing the interference activity of various fD mutants, in order to define the structural features of fD that are required for interference. A number of mutant forms of gD produced by others (G. Cohen and R. Eisenberg of the Univ. of Pennsylvania) have already been tested by others to determine whether the mutations alter gD function in the virion (function required for viral entry into cells). These same mutant forms of gD (provided by G. Cohen and R. Eisenberg) are being tested for their interference activity. Results obtained to date are summarized in FIG. 10. CHO-A12 cells, which stably express HVEM, were plated on 6-well dishes and transfected with one of several plasmids that express different forms of gD. At 24 hr after transfection, the cells were replated in 96-well plates and 12 hr later they were exposed to HSV-1(KOS)gL86 at several concentrations. At 6 hr after adding virus, the cells were solubilized and  $\beta$ -galactosidase substrate was added. The colored product was quantitated by spectromophotometry. Selecting the values obtained (OD410) at a dose of virus where the amount of virus added was directly proportional to the amount of  $\beta$ -galactosidase detected, the data were normalized for comparison by dividing the b-values obtained for cells transfected with a gD-expressing plasmid by the value obtained for cells transfected with a control plasmid (control). The forms of gD expressed by the various plasmids were wild-type gD-1 (pRE4), which is 369 amino acids in length, wild-type gD-2 (pWW65), mutant gD-1 deleted for amino acids 196-207 (pWW13), mutant gD-1 deleted for amino acids 234-244 (pWW17), mutant gD-1 deleted for amino acids 194-287 (pWW49), mutant gD-1 deleted for amino acids 234-287

(pWW52), mutant gD-1 deleted for amino acids 208-287 (pWW61), mutant gD-1 with a substitution that replaces Glu with Asp at position 63 (pWW62), mutant gD-1 deleted for amino acids 338-369 (pWW63) and mutant gD-1 with a substitution that replaces Gln with Pro at position 27 (pMW13). Low galactosidase activity implies that the transfected gD had interference activity; high activity indicates that the transfected gD had reduced or no activity. All plasmids used except pMW13 were obtained from G. Cohen and R. Eisenberg (Univ. of Pennsylvania). The results indicate that deletions or alterations of gD between the middle and membrane-spanning region of the molecule eliminate interference activity whereas deletion of the cytoplasmic tail of gD and an amino acid substitution at position 63 are without effect. An amino acid substitution at position 27 (the rid1 mutation) reduces, but does not eliminate, interference activity. From the results obtained to date, it appears that alterations affecting the function of gD in infectivity also affect its function in interference. This is consistent with the hypothesis that gD interference results from competition between cell-associated gD and virion-associated gD for a common target, possibly HVEM.

An HVEM polypeptide of the present invention has numerous uses. By way of example, such a polypeptide can be used in a screening assay for the identification of drugs or compounds that inhibit or augment the action of HVEM (e.g., agonist and antagonist to HSV entry into a cell). A screening assay for the identification of such compound, therefore, can be established whereby the ability of a compound to alter the action of HVEM can be determined by exposing cells to HSV in the presence of a polypeptide of the present invention and varying amounts of compounds suspected of inhibiting the activity of HVEM.

The hybrid protein HVEM/Fc is being used to immunize rabbits for the production of polyclonal antisera specific for the HVEM portion of the molecule. In addition the hybrid protein is used to screen for hybridomas secreting antibodies specific for the HVEM portion (the mice were immunized with HVEM-expressing CHO cells). The hybrid protein is used to determine whether a physical interaction between the hybrid protein and gD or other viral proteins can be detected. The hybrid protein also has use in screening expression cDNA libraries for natural ligands of HVEM and screening compounds for inhibitors of the interaction between HSV virions and HVEM.

In addition, an HVEM polypeptide of the present invention can be used to produce antibodies that immunoreact specifically with HVEM. Means for producing

antibodies are well known in the art. An antibody directed against HVEM can be a polyclonal or a monoclonal antibody.

Antibodies against HVEM can be prepared by immunizing an animal with an HVEM polypeptide of the present invention. Means for immunizing animals for the production of antibodies are well known in the art. By way of example, a mammal can be injected with an inoculum that includes a polypeptide as described herein above. The polypeptide can be included in an inoculum alone or conjugated to a carrier protein such as keyhole limpet hemocyanin (KLH). The polypeptide can be suspended, as is well known in the art, in an adjuvant to enhance the immunogenicity of the polypeptide. Sera containing immunologically active antibodies are then produced from the blood of such immunized animals using standard procedures well known in the art.

The identification of antibodies that immunoreact specifically with HVEM is made by exposing sera suspected of containing such antibodies to a polypeptide of the present invention to form a conjugate between antibodies and the polypeptide. The existence of the conjugate is then determined using standard procedures well known in the art.

An HVEM polypeptide of the present invention can also be used to prepare monoclonal antibodies against HVEM and used as a screening assay to identify such monoclonal antibodies. Monoclonal antibodies are produced from hybridomas prepared in accordance with standard techniques such as that described by Kohler et al. (Nature, 256:495, 1975). Briefly, a suitable mammal (e.g., BALB/c mouse) is immunized by injection with a polypeptide of the present invention. After a predetermined period of time, splenocytes are removed from the mouse and suspended in a cell culture medium. The splenocytes are then fused with an immortal cell line to form a hybridoma. The formed hybridomas are grown in cell culture and screened for their ability to produce a monoclonal antibody against HVEM. Screening of the cell culture medium is made with a polypeptide of the present invention.

#### IV. Method of Making HVEM

In another, aspect, the present invention provides a process of making HVEM. In accordance with that process, a suitable host cell is transformed with a polynucleotide of the present invention. The transformed cell is maintained for a period of time sufficient for expression of the HVEM. The formed HVEM is then recovered.

Means for transforming host cells in a manner such that those cells produce recombinant polypeptides are well known in the art. Briefly, a polynucleotide that encodes the desired polypeptide is placed into an expression vector suitable for a given host cell. That vector can be a viral vector, phage or plasmid. In a preferred embodiment, a host cell used to produce HVEM is an eukaryotic host cell and an expression vector is an eukaryotic expression vector (i.e., a vector capable of directing expression in a eukaryotic cell). Such eukaryotic expression vectors are well known in the art.

In another embodiment, the host cell is a bacterial cell. An especially preferred bacterial cell is an *E. coli*. Thus, a preferred expression vector is a vector capable of directing expression in *E. coli*.

A polynucleotide of an expression vector of the present invention is preferably operatively associated or linked with an enhancer-promoter. A promoter is a region of a DNA molecule typically within about 100 nucleotide pairs in front of (upstream of) the point at which transcription begins. That region typically contains several types of DNA sequence elements that are located in similar relative positions in different genes. As used herein, the term "promoter" includes what is referred to in the art as an upstream promoter region or a promoter of a generalized RNA polymerase transcription unit.

Another type of transcription regulatory sequence element is an enhancer. An enhancer provides specificity of time, location and expression level for a particular encoding region (e.g., gene). A major function of an enhancer is to increase the level of transcription of a coding sequence in a cell that contains one or more transcription factors that bind to that enhancer. Unlike a promoter, an enhancer can function when located at variable distances from a transcription start site so long as the promoter is present.

As used herein, the phrase "enhancer-promoter" means a composite unit that contains both enhancer and promoter elements. An enhancer promoter is operatively linked to a coding sequence that encodes at least one gene product. As used herein, the phrase "operatively linked" or its grammatical equivalent means that a regulatory sequence element (e.g. an enhancer-promoter or transcription terminating region) is connected to a coding sequence in such a way that the transcription of that coding sequence is controlled and regulated by that enhancer-promoter. Means for operatively linking an enhancer-promoter to a coding sequence are well known in the art.

An enhancer-promoter used in an expression vector of the present invention can be any enhancer-promoter that drives expression in a host cell. By employing an

enhancer-promoter with well known properties, the level of expression can be optimized. For example, selection of an enhancer-promoter that is active in specifically transformed cells permits tissue or cell specific expression of the desired product. Still further, selection of an enhancer-promoter that is regulated in response to a specific physiological signal can permit inducible expression.

A coding sequence of an expression vector is operatively linked to a transcription terminating region. RNA polymerase transcribes an encoding DNA sequence through a site where polyadenylation occurs. Typically, DNA sequences located a few hundred base pairs downstream of the polyadenylation site serve to terminate transcription. Those DNA sequences are referred to herein as transcription-termination regions. Those regions are required for efficient polyadenylation of transcribed messenger RNA (mRNA). Enhancer-promoters and transcription-terminating regions are well known in the art. The selection of a particular enhancer-promoter or transcription-terminating region will depend, as is also well known in the art, on the cell to be transformed.

A clone of the human form of HVEM was identified by DNA sequence analysis as set forth above. This clone was used in all subsequent expression studies. HVEM was expressed in CHO-K1 cells under the control of a human cytomegalovirus promoter.

Expression vectors containing the encoding DNA sequence for all or a portion of human HVEM are designated pBEC580, pBEC10, and pBL58. Both vectors were deposited, under the terms of the Budapest Treaty, on July 28, 1995 in the American Type Culture Collection, 12301 Parklawn Drive, Rockville, MD 20852, and have been assigned ATCC Accession Nos: 97236 (pBEC580), 97235 (pBEC 10), and 97237 (pBL58).

The present invention also contemplates a host cell transformed with a polynucleotide or expression vector of this invention. Means for transforming cells and polynucleotides and expression vectors used to transform host cells are set forth above. Preferably, the host cell is an eukaryotic host cell such as a mammalian cell or a prokaryotic cell such as an *E. coli*.

## V. Pharmaceutical Compositions

✓ The present invention also provides a pharmaceutical composition comprising a polypeptide or a polynucleotide of this invention and a physiologically acceptable diluent.



In a preferred embodiment, the present invention includes one or more antisense oligonucleotides or polypeptides, as set forth above, formulated into compositions together with one or more non-toxic physiologically tolerable or acceptable diluents, carriers, adjuvants or vehicles that are collectively referred to herein as diluents, for parenteral injection, for oral administration in solid or liquid form, for rectal or topical administration, or the like.

The compositions can be administered to humans and animals either orally, rectally, parenterally, intracisternally, intravaginally, intraperitoneally, locally, or as a buccal or nasal spray.

Compositions suitable for parenteral administration can comprise physiologically acceptable sterile aqueous or non-aqueous solutions, dispersions, suspensions or emulsions and sterile powders for reconstitution into such sterile solutions or dispersions. Examples of suitable diluents include water, ethanol, polyols, suitable mixtures thereof, vegetable oils and injectable organic esters such as ethyl oleate. Proper fluidity can be maintained, for example, by the use of a coating such as lecithin, by the maintenance of the required particle size in the case of dispersions and by the use of surfactants.

Compositions can also contain adjuvants such as preserving, wetting, emulsifying, and dispensing agents. Prevention of the action of microorganisms can be insured by various antibacterial and antifungal agents, for example, parabens, chlorobutanol, phenol, sorbic acid, and the like. It may also be desirable to include isotonic agents, for example, sugars, sodium chloride and the like. Prolonged absorption of the injectable pharmaceutical form can be brought about by the use of agents delaying absorption, for example, aluminum monostearate and gelatin.

Besides such inert diluents, the composition can also include sweetening, flavoring and perfuming agents. Suspensions, in addition to the active compounds, may contain suspending agents, as for example, ethoxylated isostearyl alcohols, polyoxyethylene sorbitol and sorbitan esters, microcrystalline cellulose, aluminum metahydroxide, bentonit, agar-agar and tragacanth, or mixtures of these substances, and the like.

The invention has been described in terms of preferred embodiments. One of ordinary skill in the art readily appreciates that changes and modifications can be made to those embodiments without departing from the true scope of this invention.

### Deposit

Under the terms of the Budapest Treaty on the international Recognition of the Deposit of Microorganisms for the Purpose of Patent Procedure, deposit of the plasmids pBEC10, pBEC580 and pBL58 has been made on July 28, 1995, with the American Type Culture Collection (ATCC) of Rockville, Maryland, USA, where the deposits were given ATCC accession Numbers ATCC 97235, ATCC 97236 and ATCC 97237, respectively.

Applicant's assignee, Northwestern University, represents that the ATCC is a depository afforded permanence of the deposit and ready accessibility thereto by the public if a patent is granted. All restrictions on the availability to the public of the material so deposited will be irrevocably removed upon granting of a patent. The material will be readily available during the pendency of the patent application to one determined by the Commissioner to be entitled thereto under 37 C.F.R. § 1.14 and 35 U.S.C. § 122. The deposited material will be maintained with all the care necessary to keep it viable and uncontaminated for a period of at least five years after the most recent request for the furnishing of a sample of the deposited material, and in any case, for a period of at least thirty (30) years after the date of the deposit or for the enforceable life of the patent, whichever period is longer. Applicant's assignee acknowledges its duty to replace the deposit should the depository be unable to furnish a sample when requested due to the condition of the deposit.